

Genetic analysis of lactation consistency using daily milk weights in U.S. Holsteins

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The ability of a dairy cow to perform similarly across time is an interesting trait to include in dairy cattle breeding programs aimed at improving dairy cow resilience. Consistency, defined as the quality of performing as expected each day of the lactation, could be highly associated with resilience, defined as animal's ability to maintain health and performance in the presence of environmental challenges, including pathogens, heat waves, and nutritional changes. A total of 51,415,022 daily milk weights collected from 2018 to 2023 were provided for 255,191 multiparous Holstein cows milked three times daily in conventional parlor systems on farms in 32 states by Dairy Records Management Systems (Raleigh NC).

The temporal variance (TempVar) of milk yield from 5 to 305 days postpartum was computed as the log-transformed variance of daily deviations between observed and expected individual milk weights. Lower values of TempVar imply smaller day-to-day deviations from expectations, indicating consistent performance, whereas larger values indicate inconsistent performance. Expected values were obtained using three nonparametric regression models:

1. LOESS regression with a 0.75 span;
2. polynomial quantile regression using the median (0.5), and
3. polynomial quantile regression using a 0.7 quantile.

The statistical model included age at first calving and herd-year-season as fixed effects and cow as a random effect. Heritability estimates (standard errors) of consistency ranged between 0.227 (0.011) and 0.237 (0.011), demonstrating that cows are genetically predisposed to display consistent or inconsistent performance. Correlations among TempVar traits were high (0.99), indicating that the model used to calculate consistency does not alter the ranking of Predicted Transmitting Abilities (PTAs). Genetic correlations between TempVar phenotypes and milk PTAs were 0.57, while longevity traits included Productive Life (-0.38) and Livability (-0.48). Note that as lower TempVar values are indicative of more consistent animals, negative genetic correlations with longevity traits are desirable. Our results show that cows with inconsistent milk production have lower Productive Life and Livability PTAs, meaning they have a shorter productive lifespan. Correlations between PTAs for log variance of daily milk yield and PTAs for early postpartum health traits ranged from -0.41 to -0.08. Given that health traits are derived from disease resistance measurements, this indicates that more consistent cows tended to have fewer health problems. Overall, our findings suggest

Abstract

that lactation consistency can be used to select animals that maintain expected milk production performance throughout the lactation.

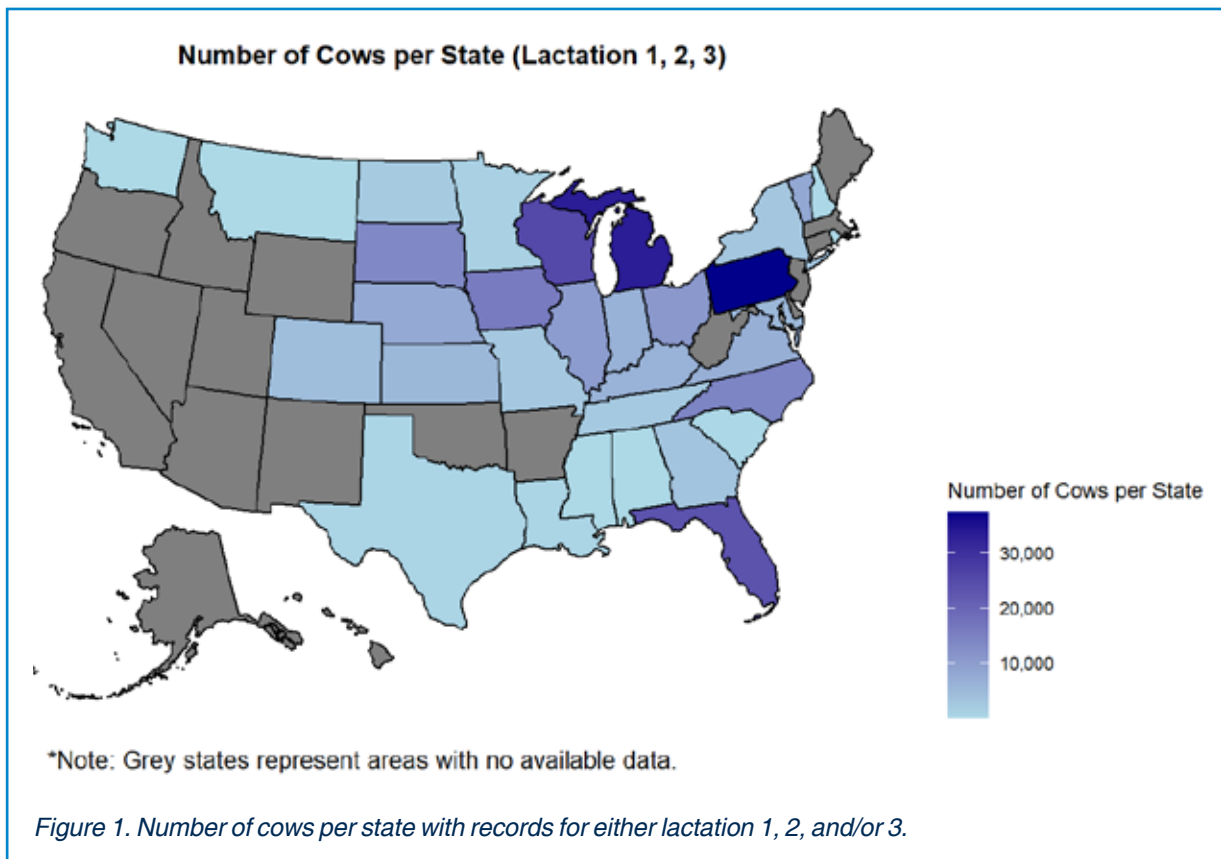
Keywords: consistency, resilience, non-parametric modelling, daily milk weights.

Introduction

The dairy industry has made enormous gains in production efficiency through improvements in genetics, nutrition, and management. Historically, genetic selection indexes emphasized increased milk production per cow, and more recently focused on improving fertility, disease resistance and feed efficiency (VanRaden *et al.*, 2021). Modern intensive farming systems have prioritized the average performance of an animal in optimal conditions, whilst ignoring the animal's ability to perform in variable or suboptimal conditions like extreme weather events, labour shortages and disease outbreaks. Resiliency is a measure of an animal's capacity to bounce back to normal functioning or maintain specific functions in the face of such environmental disturbances (Scheffer *et al.*, 2018). Resilience has been shown to be heritable in different species using high frequency daily observations such as daily milk weights (Poppe *et al.*, 2020), daily egg production (Bedere *et al.*, 2022) and daily feed intake (Putz *et al.*, 2019). Our hypothesis is that consistency is an economically important indicator of resilience. Consistency is defined as a level of performance that does not vary greatly in quality over time. The aim of this study was to calculate TempVar phenotypes using the variance of daily milk weights routinely collected on dairy farms throughout the U.S. We investigated three different methods to model individual cows' lactation curves. Genetic parameters and heritabilities of all three TempVar phenotypes, along with three different lactation stages were calculated for first parity Holstein cows. Secondly, genetic parameters, heritabilities and estimated genetic correlations among sire PTAs were calculated using a bivariate repeatability model for Holstein cows with parity 1, 2 or 3. Finally, a multi trait model was used to calculate genetic correlations between three TempVar phenotypes and economically relevant trait among different parities.

Material and methods

Data were provided by Dairy Records Management Systems (Raleigh, NC) and were extracted from PCDART on farm management software. Data were appended to a database built using the RSQLite package in R (R Project for Statistical Computing, Vienna, Austria; version 3.6.0). Individual milk weights are stored for up to 100 days while daily milk weights are stored for up to 300 days on the farm, so historical data are limited, and it was necessary to upload data from participating herds monthly and aggregate these data over time to build our SQLite research database. Data were limited to cows milked 3 times per day from 2018 to 2023 and estimated daily milk weights corresponding to days with missing values were removed. Cows milked by automatic milking systems (AMS) were excluded from the analysis. Outliers were identified and removed after decomposing the seasonal trend of the lactation curve with the Multiple Seasonal Trend decomposition method using the function `tsclean` from the `forecast` package in R (Hyndman *et al.*, 2023). `Tsclean` is a robust method to identify outliers in a univariate time series analysis using a modified Z score, in which outliers are identified based on their distance from the median (Hyndman *et al.*, 2023). Herds were required to participate in Dairy Herd Improvement (DHI) milk recording and recorded breed of cow was restricted to Holstein. After summing individual milk weights, a total of 51,415,022 daily milk weight phenotypes recorded between 5 and 305 days in milk (DIM) for 32 U.S. states remained for our analysis of milk yield TempVar (Figure 1).



The first step was to fit lactation curves using daily milk weights. Loess (span 0.75), quantile regression (0.5) and quantile regression (0.7) with a 4th order polynomial were the nonparametric methods used to model expected lactation curves. Loess is a non-parametric modelling technique to model the relationship between variables. The `quantreg` package in R (version 3.6.0) (Koenker, 2020), along with the `poly` function, was used for quantile regression analysis. Cows were required to have at least 100 aggregated daily milk weights within a lactation period to model a lactation curve. Outliers were identified and removed using the `tsclean` function from the `forecast` package in R. `Tsclean` is a robust method to identify outliers in a univariate time series analysis by using a modified Z score. The modified Z score calculates the deviation of each observation from the median, and outliers are identified based on their distance from the median relative to the median absolute deviation.

Fitting lactation curves using daily milk weights

TempVar phenotypes were calculated in two steps. First, by measuring the deviations between a cow's actual daily milk weights and her expected daily milk weights across the trajectory of her lactation, with expected values provided by the three lactation curve models described above. In the second step, the variances of these daily deviations were calculated. However, due to skewness of the distribution of variances across individual cows and lactations, a log transformation was applied to variances to derive

Calculating temporal variance phenotypes

three TempVar phenotypes, namely LnVar_loess, LnVar_qr05, and LnVar_qr07, for each method and each cow in step 2, as follows:

$$\text{daily deviation}_{ijk} = [\text{yield}_{ijk} - \widehat{\text{yield}}_{ijk}]$$

$$\text{TempVar}_{ij} = \log\{\text{Var}[\text{daily deviation}_{ijk}]\}$$

where i is the individual cow, j indicates parity and k represents DIM between 5 and 305. Thus, a consistent cow is defined by low temporal variation in actual versus predicted daily milk production throughout the lactation, and an inconsistent cow is defined by high temporal variation in actual versus predicted daily milk yield throughout the lactation.

Univariate analysis of temporal variance of milk yield in first lactation

Our initial analysis, which was restricted to first parity cows, included 20,787,272 daily milk weights from 102,216 cows in 213 herds in 30 states. Variance components and genetic parameter estimates were obtained using the AIREMLF90 software (Aguilar *et al.*, 2018). TempVar phenotypes were analyzed using the following model:

$$y_{ijkl} = AFC_i + HYS_j + a_k + e_{ijkl},$$

where y_{ijkl} is the TempVar phenotype, AFC_i is the fixed effect of age at first calving (6 levels; <=22, 23-24, 25-26, 27-28, 29-30, 30+), HYS_j is the fixed effect of herd-year-season of calving (2,347 levels, with a minimum of 5 observations per level), a_k is the random effect of cow with 102,216 levels distributed as $\mathbf{a} \sim \mathbf{N}(0, \mathbf{A}\sigma_a^2)$, and e_{ijkl} is the random residual effect distributed as $\mathbf{e} \sim \mathbf{N}(0, \mathbf{I}\sigma_e^2)$.

Univariate analysis of temporal variance of milk yield by stage of lactation

After fitting individual lactation curves for first lactation cows using LOESS and polynomial quantile regression, three different lactation stages based on DIM were considered to reflect early, mid, and late lactation. Early lactation ranged from 5 to 50 DIM, mid lactation ranged from 51 to 200 DIM, and late lactation ranged from 201 to 305 DIM. Individual cows were required to have daily milk weights spanning at least 50% of the period to be included in the analysis. In other words, at least 22 daily milk weights were required in early lactation, 75 daily milk weights were required in mid lactation, and 52 daily milk weights were required in late lactation. Consequently, a specific first parity cow could be included in the analysis for one, two, or the three periods. After edits, 66,297 cows were used to estimate genetic parameters in early lactation, 85,445 cows in mid lactation, and 71,673 cows in late lactation. Variance components and heritability estimates for LnVar_loess, LnVar_qr05, and LnVar_qr07 were calculated within each lactation period using a univariate model, and relationships across periods were assessed using Pearson's correlations of sire PTAs in different periods.

Analyses of temporal variance of milk yield across lactations

The edits described previously were subsequently applied to daily milk yield data of second and third parity cows to assess relationships in the TempVar of milk yield across parities. Cows were not required to have records in all three lactations because, given the structure of our database, the number of cows with records in multiple parities was limited. In the dataset, there were 36,589 cows with records in both parity 1 and 2. Additionally, 25,702 cows had records in both parity 2 and parity 3. Furthermore,

5,496 cows had records in both parity 1 and parity 3. Finally, there were 4,904 cows with records in all three parities (parity 1, parity 2, and parity 3). We implemented a repeatability model, as well as two bivariate models (first and second lactation, second and third lactation), using a total of 51,415,022 daily milk weights records from 106,033 first parity cows, 89,315 second parity cows and 59,843 third parity cows. These data represented 222 herds from 32 U.S. states (Figure 2). Variance components and genetic parameter estimates were obtained using the AIREMLF90 software (Aguilar *et al.*, 2018). Fixed effects included parity (3 levels), age at calving (18 levels; <=22, 23-24, 25-26, 27-28, 29-30, or 30+ months for first parity; <=35, 36-37, 38-39, 40-41, 42-43, or 44+ months for second parity, and <=47, 48-49, 50-51, 52-53, 54-55, or 56+ months for third parity), and herd-year-season (2,856 levels with ≥ 5 records per level). Cow was fitted as a random effect using up to five generations of pedigree data.

Repeatability model:

$$y_{ijklmn} = \text{Parity}_i + CA_j + HYS_k + a_l + pe_m + e_{ijklmn},$$

where y_{ijklmn} is the TempVar phenotype, Parity_i is the fixed effect lactation number with 3 levels, CA_j is the fixed effect of calving age with 18 levels, HYS_k is the fixed effect of herd calving year season with 2,856 levels, a_l is the random effect of cow with 255,191 levels distributed as $\mathbf{a} \sim N(0, \mathbf{A}\sigma_a^2)$, pe_m is the random permanent environmental effect distributed as $\mathbf{pe} \sim N(0, \mathbf{I}\sigma_{pe}^2)$, and e_{ijklmn} is the random residual effect distributed as $\mathbf{e} \sim N(0, \mathbf{I}\sigma_e^2)$.

Multiple trait model:

$$y_{ijkl} = CA_{i+} + HYS_{j+} + a_k + e_{ijk},$$

where all model terms are as described previously. The assumptions of both bivariate analyses, which were carried out using first and second lactation TempVar phenotypes or second and third lactation TempVar phenotypes, were as follows:

$$\begin{bmatrix} a_1 \\ a_2 \end{bmatrix} \sim N \left[\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_{a1}^2 & \sigma_{a12} \\ \sigma_{a12} & \sigma_{a2}^2 \end{pmatrix} \otimes A \right]$$

$$\begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \sim N \left[\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_{e1}^2 & \sigma_{e12} \\ \sigma_{e12} & \sigma_{e2}^2 \end{pmatrix} \otimes I \right]$$

where a_i is the additive genetic effects for trait i , σ_{ai}^2 is the additive genetic variance of trait i , σ_{aij} is the additive genetic covariance between trait i and j , e_i is the residual effect for trait i , σ_{ei}^2 is the residual variance of trait i , and σ_{eij} is the residual covariance between trait i and j .

Sires with ≥ 10 daughters with TempVar phenotypes (repeatability model, n=2,572) were used to calculate approximate genetic correlations between milk yield TempVar and other economically relevant traits using the Calo's method (Calo *et al.*, 1973; Blanchard *et al.*, 1983). PTAs from economically relevant traits evaluated by the Council on Dairy Cattle Breeding (Bowie, MD) were extracted from the April 2023 genetic evaluation. The approximate genetic correlations were calculated as follows:

Correlations between temporal variance of milk yield and other economically relevant traits

$$\hat{r}_{i,j} = \frac{\sqrt{\sum(Rel_i) \sum(Rel_j)}}{\sum(Rel_i Rel_j)} r_{i,j},$$

where $\hat{r}_{i,j}$ = approximate genetic correlation between traits i and j; $\sum Rel_i$ and $\sum Rel_j$ = the sum of reliabilities of traits i and j; Rel_i and Rel_j = reliabilities of traits i and j; and $r_{i,j}$ = Pearson correlation between PTA for traits i and j.

Results and discussion

Heritabilities (se) of TempVar phenotypes were moderate and ranged from 0.227 (0.011) to 0.237 (0.011) (Table 1). These heritabilities indicate two important concepts – that we can select for consistent milk performance genetically, and the non-parametric methods used to model lactation curves have little impact on our trait definition. We found differences in heritabilities among lactation stages (Table 2). In early lactation, the estimated heritabilities of TempVar phenotypes ranged from 0.129 (0.010) - 0.154 (0.011), in mid lactation heritabilities ranged from 0.190 (0.011) to 0.197(0.011) and in late lactation from 0.159 (0.011) to 0.164 (0.011). Across all three TempVar phenotypes,

Table 1. Variance components and heritability estimates (SE)¹ for temporal variance (TempVar) of daily milk yield in first parity Holstein cows over the entire lactation. TempVar phenotypes were calculated as log-transformed variances of daily deviations from lactation curves predicted with LOESS regression (0.75 span parameter) or polynomial quantile regression (0.5 or 0.7 quantile).

| Method | σ_a^2 | σ_e^2 | h^2 |
|-------------|---------------|---------------|---------------|
| LnVar_loess | 0.050 (0.002) | 0.162 (0.001) | 0.237 (0.011) |
| LnVar_qr05 | 0.052 (0.002) | 0.171 (0.002) | 0.231 (0.011) |
| LnVar_qr07 | 0.052 (0.002) | 0.176 (0.002) | 0.227 (0.011) |

¹ σ_a^2 = additive genetic variance; σ_e^2 = residual variance; h^2 = heritability.

Table 2. Phenotypic means, standard deviations (SD), variance components and heritability estimates (SE)¹ for the temporal variance (TempVar) of daily milk yield in first parity Holstein cows at 3 different lactation stages. TempVar phenotypes were calculated as log-transformed variances of daily deviations from lactation curves predicted with LOESS regression (0.75 span parameter) or polynomial quantile regression (0.5 or 0.7 quantile).

| Method | Lactation | | | σ_a^2 | σ_e^2 | h^2 |
|-------------|------------|------|------|---------------|---------------|---------------|
| | Stage | Mean | SD | | | |
| LnVar_loess | 5 to 50 | 3.95 | 0.73 | 0.046 (0.003) | 0.256 (0.003) | 0.154 (0.011) |
| | 51 to 200 | 3.53 | 0.76 | 0.046 (0.002) | 0.187 (0.002) | 0.197 (0.011) |
| | 201 to 305 | 3.42 | 0.77 | 0.043 (0.003) | 0.221 (0.002) | 0.164 (0.011) |
| LnVar_qr05 | 5 to 50 | 3.72 | 0.80 | 0.049 (0.003) | 0.312 (0.003) | 0.136 (0.010) |
| | 51 to 200 | 3.56 | 0.77 | 0.047 (0.002) | 0.196 (0.002) | 0.194 (0.011) |
| | 201 to 305 | 3.43 | 0.78 | 0.043 (0.003) | 0.225 (0.002) | 0.161 (0.011) |
| LnVar_qr07 | 5 to 50 | 3.75 | 0.81 | 0.048 (0.003) | 0.326 (0.003) | 0.129 (0.010) |
| | 51 to 200 | 3.56 | 0.77 | 0.047 (0.002) | 0.200 (0.002) | 0.190 (0.011) |
| | 201 to 305 | 3.44 | 0.78 | 0.043 (0.003) | 0.230 (0.002) | 0.159 (0.011) |

¹ σ_a^2 = additive genetic variance; σ_e^2 = residual variance; h^2 = heritability.

estimates of the additive genetic variance were highest during the period from 5 to 50 DIM. This is an interesting and promising result, as it seems to indicate that genetic differences in milk yield consistency are expressed more fully under challenging conditions, albeit with the complication of greater residual variances. Mulder *et al.* (2013) previously indicated that greater genetic variation in resilience would be observed when an animal is exposed to environmental challenges. Increased variation in daily milk production during this period may reflect the challenges of decreased voluntary feed intake, coupled with the physiological demands of rapid increases in energy requirements for milk production (White, 2015). Previous authors have described challenges such as negative energy balance (Collard *et al.*, 2000), hyperketonemia (Duffield *et al.*, 2009), and resumption of ovarian cyclicity (Gaillard *et al.*, 2016) during this period, all of which can contribute to an increase in the environmental variance. Heritabilities were lowest for LnVar_qr07 across all three lactation stages. This is most likely caused by fitting the 0.7 quantile, which reflects the animals potential milk production and could be more informative for calculating resilience indicators (Poppe *et al.*, 2020)

The assumption of the repeatability animal model is that the genetic correlation between records is equal to 1, indicating that TempVar traits are genetically identical across parities. In table 4, genetic correlations among different parities for each TempVar phenotype are shown. Genetic correlations (se) ranged from 0.963 (0.010) to 0.999 (0.003) which indicated that consistency is the same trait regardless of parity. Repeatability (se) ranged from 0.331 (0.003) to 0.341 (0.003) indicating that the genetic influence on consistent performance is relatively stable and repeatable over time, suggesting that selection for that trait is likely to be effective (Table 3). Because first lactation cows are immature and still growing, many traits are genetically or physiologically distinct between primiparous and multiparous cows. Therefore, we decided to estimate heritability, repeatability, and genetic correlations of TempVar phenotypes in first, second, and third parities. Heritability estimates were slightly lower when calculated using the repeatability model, but relatively few cows had TempVar phenotypes for multiple parities, because daily milk yield records from cows that calved prior to initiation of our research database were unavailable. Genetic correlations among TempVar phenotypes were >0.95 between parities (Table 4), indicating that TempVar phenotypes are genetically quite similar throughout the cow's life, and suggesting that we should consider milk yield consistency as the same trait across lactations.

Table 3. Variance components and heritability estimates (SE)¹ for the temporal variance (TempVar) of daily milk yield using a repeatability model applied to full lactation data of cows with records in lactation 1, 2 and/or 3. TempVar phenotypes were calculated as log-transformed variances of daily deviations from lactation curves predicted with LOESS regression (0.75 span parameter) or polynomial quantile regression (0.5 or 0.7 quantile).

| Method | σ_a^2 | σ_{pe}^2 | σ_e^2 | h^2 | r^2 |
|-------------|---------------|-----------------|---------------|---------------|---------------|
| LnVar_loess | 0.052 (0.001) | 0.026 (0.001) | 0.151 (0.001) | 0.227 (0.006) | 0.341 (0.003) |
| LnVar_qr05 | 0.053 (0.001) | 0.026 (0.001) | 0.158 (0.001) | 0.222 (0.006) | 0.339 (0.003) |
| LnVar_qr07 | 0.053 (0.001) | 0.028 (0.001) | 0.164 (0.001) | 0.216 (0.006) | 0.331 (0.003) |

¹ σ_a^2 = additive genetic variance; σ_{pe}^2 = permanent environmental variance; σ_e^2 = residual variance; h^2 = heritability; r^2 = repeatability.

Table 4. Variance components and heritability estimates (SE) using a multiple-trait model applied to full lactation data of cows with records in lactation 1, 2 and/or 3. Phenotypes representing the temporal variance in daily milk yield were calculated as log-transformed variances of daily deviations from lactation curves predicted with LOESS regression (0.75 span parameter) or polynomial quantile regression (0.5 or 0.7 quantile).

| Lactation | No. of cows | Method | | |
|-----------|-------------|---------------|---------------|---------------|
| | | LnVar_loess | LnVar_qr05 | LnVar_qr07 |
| 1 and 2 | 195,348 | 0.976 (0.006) | 0.977 (0.006) | 0.978 (0.006) |
| 1 and 3 | 165,876 | 0.963 (0.010) | 0.963 (0.010) | 0.964 (0.010) |
| 2 and 3 | 149,158 | 0.998 (0.003) | 0.999 (0.003) | 0.999 (0.003) |

Table 5. Correlations estimated using the Calo's method between sire PTAs for temporal variance (TempVar) of daily milk yield and other economically relevant traits. PTAs for TempVar were obtained for sires with ≥ 10 daughters using a repeatability model applied to full lactation data of cows with records in lactation 1, 2 and/or 3. PTAs for production, longevity, fertility, health, and efficiency were retrieved from the April 2023 National Genetic Evaluation generated by the Council on Dairy Cattle Breeding. TempVar phenotypes were calculated as log-transformed variances of daily deviations from lactation curves predicted with LOESS regression (0.75 span parameter) or polynomial quantile regression (0.5 or 0.7 quantile).

| Trait | Method | | |
|-----------------------------|-------------|------------|------------|
| | LnVar_loess | LnVar_qr05 | LnVar_qr07 |
| Milk (lb) | 0.57 | 0.57 | 0.57 |
| Fat (lb) | 0.11 | 0.11 | 0.11 |
| Protein (lb) | 0.39 | 0.39 | 0.39 |
| Productive Life (months) | -0.38 | -0.38 | -0.38 |
| Livability | -0.48 | -0.48 | -0.48 |
| Heifer Livability | -0.04 | -0.04 | -0.04 |
| Daughter Pregnancy Rate (%) | -0.42 | -0.42 | -0.42 |
| Heifer Conception Rate (%) | -0.20 | -0.20 | -0.20 |
| Cow Conception Rate (%) | -0.41 | -0.41 | -0.41 |
| Gestation Length | -0.02 | -0.02 | -0.02 |
| Early First Calving | 0.06 | 0.05 | 0.05 |
| Somatic Cell Score | 0.26 | 0.27 | 0.27 |
| Milk Fever | -0.08 | -0.08 | -0.08 |
| Displaced Abomasum | -0.25 | -0.25 | -0.25 |
| Ketosis | -0.28 | -0.28 | -0.29 |
| Mastitis | -0.41 | -0.42 | -0.42 |
| Metritis | -0.21 | -0.20 | -0.20 |
| Retained Placenta | -0.10 | -0.10 | -0.10 |
| Residual Feed Intake | 0.05 | 0.05 | 0.05 |
| Feed Saved | -0.05 | -0.04 | -0.04 |

Estimated genetic correlations showed favourable relationships between TempVar phenotypes and several traits included in the U.S. Net Merit selection index. Interestingly, the correlation between TempVar phenotypes and milk was 0.57 indicating that as milk production increases, TempVar phenotypes increase. This reflects the scaling relationship between mean and variance where we expect milk yield and TempVar PTAs to increase simultaneously. Interestingly, for all health-related traits, the estimated genetic correlations among sire PTAs were negative. Specifically, for displaced abomasum, ketosis, mastitis, and metritis we found moderate correlations ranging from -0.21 to -0.42. Correlations between TempVar phenotypes and somatic cell score (SCS) ranged from 0.26 to 0.27, which is also favourable as a higher SCS indicates higher levels of mastitis (Table 5). This is logical, because consistent cows will tend to have fewer disease events, fewer visits to the hospital pen, and fewer management interventions that may cause fluctuations in daily milk yield. The strongest correlations observed in this study were between milk yield TempVar and mastitis, presumably because mastitis is a common disease that causes large decreases in milk production (Liang *et al.*, 2017; Seegers *et al.*, 2003). Overall, lower temporal variance (consistent performance) was associated with superior health, longevity, and fertility. It should be noted that, while we required a minimum of 100 daily milk weights to compute TempVar phenotypes in the present study, we recognize that fragile cows with health or fertility problems may get culled at a higher rate than resilient cows, and we should therefore recognize that improvements in generalized resilience will likely come from a selection index containing PTAs for milk yield TempVar, longevity, and early postpartum health disorders. Correlations of TempVar traits with feed efficiency were near zero, suggesting that selection for lower residual feed intake and greater feed saved will increase farm profitability (Parker Gaddis *et al.*, 2021) with no adverse impacts on resilience.

This study aimed to examine the genetics of milk yield consistency within and between lactations of U.S. Holstein cows. Our findings suggest that TempVar is moderately heritable, which may allow selection to focus on cows with smaller fluctuations in daily milk yields throughout lactation than their contemporaries. TempVar phenotypes appear to be robust to the choice of lactation curve models, and genetic rankings seem to be consistent across lactations. Cows displaying superior milk yield consistency tend to be genetically superior for productive life, female fertility, and resistance to early postpartum health disorders relative to their inconsistent contemporaries. Definition of consistency phenotypes and characterization of their genetic basis is an important initial step in developing resilience indicators that will allow selection for consistent performance in unpredictable conditions. Improving resilience will lead to improvements in dairy farm profitability, reduce animal health and welfare risks associated with management and weather disturbances, and improve the social and environmental sustainability of dairy farming.

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Conclusions

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